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Short Synopsis

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Title: MATHEMATICAL MODELING ON COMMUNICABLE DISEASE

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ABSTRACT

Mathematical modelling is the process of constructing, improving and testing the mathematical model in the various problems of biology. There are many possibilities to improve the model using real world parameters, exist for research level. This work emphasizes to understand the population dynamics of infection through mathematical models. Under the consideration of real life parameters a new mathematical models provides a qualitative approach for better representation of different infectious disease. The result of improved mathematical models approaches an evaluation of prevention, control and treatment of infectious diseases.

Keywords: Epidemic Disease, Mathematical Modelling, Differential Equation, Ecology, Bio-Mathematics.

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1. INTRODUCTION

"Mathematical biology" is a fast-developing, well defined subject and the most exciting application of modern ages of the applied mathematics.

The increasing wide scope of biomathematics is unavoidable as biology becomes highly qualitative as well as quantitative. The complex nature of the biological sciences makes an interdisciplinary involvement essential. For a person from the background of science, scientist, mathematician, biology, opens new and exciting branches, also for the new researchers in the field of biology. Mathematical modelling provides another research tool which commensurate with a new powerful laboratory technique.

Epidemiology is the subject that studies the spread of diseases in the human populations. Mathematical epidemiology is concerned with the quantitative aspects of the subject. Often the work of a mathematical epidemiologist consists of

i. building of model with a various parameters,
ii. estimation of parameters,
iii. investigation of the sensitivity of the model with a various number's of parameters,
iv. Simulations analysis.

All these activities are expected to tell us something about the spread of the disease in the human population, the possibility to control this spread and how to make the model that the disease disappear from the human population.

Although many people are familiar with the world "virus" but only few people have awareness about the characteristics of virus. It is composed of eight single stranded segments of RNA wound helically and associated with protein to from a nucleocapsid. The virus envelope contains a series of projections called spikes. The spikes contain the enzymes hemagglutinin (H) and neuraminidase (N), which assist the entry of the virus into its host cell while *Bacteria* :Bacteria are the cells of small size, found in the environment as either individual or aggregated cells together as clumps, and their intracellular structure is much simpler than eukaryotes. Bacteria have a single circular DNA chromosome that is found within the cytoplasm of the cell as they do not have a nucleus. Although bacteria are Prokaryotic, Microscopic, single cells, size 0.2 to 2.0 micrometers in diameter, 2 to 8 micrometers in length and usually have a cell wall.

The main problem is to describe by the mathematical modelling with a differential equation on infectious disease. The basic problem has been taken to discuss the spread of an infectious disease within a population.

In mathematical modelling, first formulate the model and its consequences can be deduced by using mathematical techniques and the result can be compared with the past observations. Mathematical model, which is based on differential equations in the proposed research work solve by using the MATLAB software. The main focus is to present a model of quantitative predictions for Prevention and Medication.

2. LITERATURE REVIEW

Diána H. Kniplet. al. 2011, presented the basic SIR model, the basic reproduction number denoted by R_0, is one of the most important parameters of an epidemic and Influenza models - asymptomatic infection, vaccination and antiviral treatment.

G. Abramson et.al. 2001, discussed four sections as non-extended models in Section 1 and extended models in Section 2, constitute the classical theory of epidemic spread while Section 3 introduces complex networks and epidemics on complex networks is given in Section 4. H.P. Duerret. al. 2007, discussed modelling approach to pandemic influenza, various contact networks and identify appropriate strategies of disease control measures.

Herbert W. Hethcoteet. al. 2000 presented the mathematical models MSEIR and SEIR endemic models and calculates the values of the basic reproduction number for various diseases.

Influenza, World Health Organization, April 2009. Available from: *http://www.who.int/mediacentre/factsheets/fs211/en/*, 2012 shows the updated information on influenza.

J.D. Murray, et. al. 2001 published in his book "Mathematical Biology" described Discrete and Continuous Population Models for Single Species, Modelling the Dynamics of Marital Interaction: Reaction Kinetics, Biological Oscillators and Switches, BZ Oscillating Reactions, Perturbed and Coupled Oscillators and Black Holes, Dynamics of Infectious Diseases, Reaction Diffusion, Chemo taxis, and Nonlocal Mechanisms, Oscillator-Generated Wave Phenomena.

John D. Mathews et. al. 2007, provided evaluation of the basic reproduction number for the bio mathematical model and discussed the prior immunity, asymptomatic infection and waning time and the Markov Chain Monte Carlo fitting algorithm.

S. Levin 1986, presented Lecture on Biomathematics, This paper is an expository and nontechnical review of some recent discoveries about food webs.

Jeffery K. Taubenberger et. al. 2006 "1918 Influenza: the Mother of All Pandemics" analysed the 1918 pandemic and its implications for future pandemics, which requires careful experimentation with through study, Emerging Infectious Diseases.

J. N. Kapur, et.al. 2010 published in his book "Mathematical models in Biology & Medicine" a large number of bio mathematical techniques have been developed till now to get an insight into the complex biological, ecological, and physiological situations. A variety of mathematical techniques have been employed to solve these models. M. Derouich, A. Boutayebet. al. 2006, his work on "Dengue fever: Mathematical modelling and computer simulation" and represented the explanation of stability for the equilibrium points is carried out and a simulation for a various parameter settings. M. Derouich and A. Boutayebet. al. 2008, studied about the mathematical modelling with an avian influenza. The model consists of ordinary differential equations, stability analysis, simulation and matrix of linearization. Also, this method shows the behaviour of the disease by simulation with different parameters values. Murali Haran et. al. 2009, discussed on some simple deterministic models, simple stochastic models, some simple spatial (dynamic) models.

M. Iannelliet. al. 2005 used mathematical modelling of epidemics and discussed herd immunity and reproduction number R_0 to determine a threshold for two alternatives disease free equilibrium and endemic equilibrium.

Matthew James Keeling and Pejman Rohaniet. al. 2008, describe the modelling on an infectious diseases in humans and animals.

M. Martchevaet. al. 2011, presented a research paper on "Avian Flu: influenza is a zoonotic disease where the transmission occurs from infected domestic birds to human populations and described a mathematical models, the basic reproduction number, control measures, mathematical epidemiology.

Ministry of Health and Family Welfare, 2011 provided the information on Swine Flu.

Nature outlook: Influenza/11 Dec.2011/vol.480/Issue No. 7376, shows the present and past history of influenza. Also, gives the latest news and research on influenza and vaccine for all seasons. P. Paleseet. al. 1982 provided the variation in all types of influenza infection and the mechanism responsible for changes in these viruses are not well defined.

Renato Casagrandiet. al 2005, developed a simple mathematical model to analyse the epidemiological consequences of the drift mechanism for influenza A virus, which was an improvement over the SIR model. S. J. Chapman et. al. 2009, presented the benefits of mathematical modelling which are highlighted, and the need for multiscale models in medicine and biology. S. Seddighiet. al. 2009 discussed Threshold Conditions in SIR STD Models, different constraint; Reproductive number; Sensitivity and Transmission. W. Chinviriyasitet. al. 2007 presented a numerical modelling of the transmission dynamics of influenza with SIRC model and discussed the convergence to the true steady state for any time step used and also produced solutions to the seasonal SIRC model, which were similar to reported in Casegrandiet. al. 2006. Baris Hanciogluet. al. 2006, presented a dynamical model of immune response to uncomplicated influenza virus infection, which analysis on the control of the disease by the innate and adaptive immunity and analysed it's behaviour. This model is used to provide the experimental trials of antiviral strategies in genetically heterogeneous hosts and to construct response surfaces to be integrated in multi-scale models of influenza A virus infection (Clermont et.al. 2004). C.M. Pease, 1987, explains the evolutionary mechanism for the study of epidemic disease viz. influenza A virus. In the non-evolutionary models, susceptible are continually introduced into the host population by demographic processes: most hosts that die are immune, while new born hosts are susceptible show how the non-dimensional parameter E = myN/r' may be calculated from four types of data.

The description and analyses of the model on infectious diseases, which calculate susceptibility and immunity of an infected person and other conditions like as emigration or migration for characterization of the model, where the epidemic will spread.

3. DESCRIPTION OF BROAD AREA

Anumber of solutions of the governing equations are obtained. Here, in order to obtain the value of the parameters and constant, we merely substitute the initial condition into the set of solutions. Which is provided by an initial value problem, including compartmental model and population growth models etc.

i. Simple SIR dynamic model used to determine the basic reproduction number for study of the immune system.

ii. Mathematical model with threshold can be determine the stability with the help of initial value problem with the LPP or Numerical Methods (e.g. Runga Kutta method etc.) and discuss its convergence.

iii. Statistical models will define the relationship between the different "parameters and constants" and compute optimize value and also compares outcome from the others observations.

The model predicts that the prevalence of a virus is very high an intermediate value of the basic reproduction number via a bifurcation analysis of the model. The effect of seasonal infection on the epidemiology regimes. Construction of the simple governing equations to analysis the epidemiological consequences of the drift mechanism for epidemic diseases.

4. OBJECTIVE OF THE RESEARCH WORK

(1) The objective of the study is to create a model which will be helpful in controlling the communicable disease.

(2) To develop a new mathematical concept or technique through which can prevent and medicate the communicable disease.

(3) To analyse the data from real phenomena and obtain the sound conclusions about the underlying processes using their understanding of mathematical backgrounds.

(4) To motivate and develop a various mathematical and statistical models for many biological problems drawn from real situations.

(5) To analyse how mathematics, statistics and computing can be used in an integrated way to analyse the bio-mathematical problems.

5. METHODOLOGY

In this research, the useful sources are:

(1) Classical mathematical techniques, which include Ordinary Differential equation, Partial Differential equations, Integro-differential equations, Delay Differential equations, difference equations etc.

(2) Computer techniques, which include MATLAB or Mathematica to solve the equations developed by modelling.

(3) (i) Digital Library – Manav Rachna International University, Faridabad.

(ii) National Medical Library - AIIMS, New Delhi.

(4) Steps to be followed during research work are:

(i) To learn more study of the topic.

(ii) To visit to the Library and Hospitals/Clinics to collect the data.

(iii) Model execution with the collected data from hospital/Clinics and library.

(iv) To learn to build the new mathematical model.

(v) To learn MATLAB software to solve complicated numerical system.

(vi) Implementation and improvement of Mathematical model with different parameters.

(vii) Study of some important diagnostic fields using the model output.

(5) Modified the SIR model into many different mathematical models. For example, if consider the SIR model. Then the differential equations of SIR models given as follows:

$$\frac{dS}{dt} = -\beta C \frac{SI}{N} \qquad \text{(i)}$$

$$\frac{dI}{dt} = \beta C \frac{SI}{N} - \gamma I \qquad \text{(ii)}$$

$$\frac{dR}{dt} = \gamma I \qquad \text{(iii)}$$

Where S = Susceptible, I = Infection, R = Immune (removed), t = time and N = S+I+R = Constant.

6. EXPECTED OUTCOMES OF THE RESEARCH

(1) In this research, a kind of mathematical model is developed, which will use the sufficient numbers of parameters in the model and will able to control the number of infected patients which is seasonally or non-seasonally infected. This can be done by using various factors affecting by the communicable disease which include prevention and medication etc.

(2) The basic concepts of infectious disease transmission and control and the distinguish between infectious diseases and non-infectious diseases.

(3) Policy-makers and disease-control agencies who want to

- set appropriate goals for and check the performance of infection-control plan;
- Interpret the findings of mathematical modeling polices.

(4) All who want to use the new techniques of analysis in the field of epidemiology and control of infectious diseases, in medical field.

(5) Health economists who want to develop appropriate models of infectious-disease control strategies.

(6) Researchers who want experience of using modern quantitative approaches to infectious disease epidemiology.

(7) Professionals planning for the control of a deliberately or accidentally released pathogen.

(8) Mathematicians who want to study the biological backgrounds and apply it for the construction of bio-mathematical modeling to understand the new era.

(9) The population models will give an idea of the future that how many people will be suffering from communicable disease so that proper medication and facilities can be provided and research can be done in this area to control the increasing infected population and hence it will be very helpful in the field of medical science and also an ordinary man can understand it in an easy manner through presentation.

7. Proposed Time Frame (Gantt Chart)

Year	**Plan of Research Work**
1st Year	Course work & Literature Survey
2nd Year	Hospital/lab visited for Data Collection &Creating models with different Parameters
3rd Year	Analysis & Publishing Research Work
4th Year	Thesis Writing and Submission

Work ↓ / Time →	1st Year		2nd Year		3rd Year		4th Year	
	Six months	Six months	Six months	Six months	Six months	Six months	Six months	Six months
Course work & Literature Survey	←	→						

Hospital/lab visited for Data Collection & Creating models with different Parameters			←	—	→		
Analysis & Publish Research Work				←	—	→	
Thesis Writing and Submission					←	—	→

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